IFWO

**RAW SEQUENCE LISTING** DATE: 09/16/2004
PATENT APPLICATION: **US/10/774,176** TIME: 12:15:26

Input Set : **N:\Crf3\RULE60\10774176.raw**
Output Set: **N:\CRF4\09162004\J774176.raw**



```
 1 <110> APPLICANT: CARROLL, MILES WILLIAM
 2       MYERS, KEVIN ALAN
 3 <120> TITLE OF INVENTION: POLYPEPTIDE
 4 <130> FILE REFERENCE: 078883/0120
 5 <140> CURRENT APPLICATION NUMBER: US/10/774,176
 6 <141> CURRENT FILING DATE: 2004-02-06
 7 <150> PRIOR APPLICATION NUMBER: US/09/533,798
 8 <151> PRIOR FILING DATE: 2000-03-24
 9 <150> PRIOR APPLICATION NUMBER: 60/126,187
10 <151> PRIOR FILING DATE: 1999-03-25
11 <150> PRIOR APPLICATION NUMBER: 60/126,188
12 <151> PRIOR FILING DATE: 1999-03-25
13 <150> PRIOR APPLICATION NUMBER: GB 9825303.2
14 <151> PRIOR FILING DATE: 1998-11-18
15 <150> PRIOR APPLICATION NUMBER: GB 9901739.4
16 <151> PRIOR FILING DATE: 1999-01-27
17 <150> PRIOR APPLICATION NUMBER: GB 9917995.4
18 <151> PRIOR FILING DATE: 1999-07-30
19 <160> NUMBER OF SEQ ID NOS: 27
20 <170> SOFTWARE: PatentIn version 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1263
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1
27       atgcctgggg ggtgctcccg gggccccgcc gccggggacg ggcgtctgcg gctggcgcga     60
28       ctagcgctgg tactcctggg ctgggtctcc tcgtcttctc ccacctcctc ggcatcctcc    120
29       ttctcctcct cggcgccgtt cctggcttcc gccgtgtccg cccagccccc gctgccggac    180
30       cagtgccccg cgctgtgcga gtgctccgag gcagcgcgca cagtcaagtg cgttaaccgc    240
31       aatctgaccg aggtgcccac ggacctgccc gcctacgtgc gcaacctctt ccttaccggc    300
32       aaccagctgg ccgtgctccc tgccggcgcc ttcgcccgcc ggccgccgct ggcggagctg    360
33       gccgcgctca acctcagcgg cagccgcctg gacgaggtgc gcgcgggcgc cttcgagcat    420
34       ctgcccagcc tgcgccagct cgacctcagc cacaacccac tggccgacct cagtcccttc    480
35       gctttctcgg gcagcaatgc cagcgtctcg gcccccagtc cccttgtgga actgatcctg    540
36       aaccacatcg tgccccctga agatgagcgg cagaaccgga gcttcgaggg catggtggtg    600
37       gcggccctgc tggcgggccg tgcactgcag gggctccgcc gcttggagct ggccagcaac    660
38       cacttccttt acctgccgcg ggatgtgctg gcccaactgc ccagcctcag gcacctggac    720
39       ttaagtaata attcgctggt gagcctgacc tacgtgtcct tccgcaacct gacacatcta    780
40       gaaagcctcc acctggagga caatgccctc aaggtccttc acaatggcac cctggctgag    840
41       ttgcaaggtc taccccacat tagggtttte ctggacaaca atccctgggt ctgcgactgc    900
42       cacatggcag acatggtgac ctggctcaag gaaacagagg tagtgcaggg caaagaccgg    960
43       ctcacctgtg catatccgga aaaaatgagg aatcgggtcc tcttggaact caacagtgct   1020
44       gacctggact gtgacccgat tcttccccca tccctgcaaa cctcttatgt cttcctgggt   1080
```

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attgttttag ccctgatagg cgctattttc ctcctggttt tgtatttgaa ccgcaagggg 1140
ataaaaaagt ggatgcataa catcagagat gcctgcaggg atcacatgga agggtatcat 1200
tacagatatg aaatcaatgc ggaccccaga ttaacaaacc tcagttctaa ctcggatgtc 1260
tga 1263

<210> SEQ ID NO: 2
<211> LENGTH: 1281
<212> TYPE: DNA
<213> ORGANISM: Mus musculus
<400> SEQUENCE: 2
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ctggcgctag tgctgctggg ttgggtctcc gcgtcggccc ccagctcttc ggtaccctcg 120
tcttccacct ccccggcaga cttcctggcc tcggggtctg cgcagcctcc gccagccgag 180
agatgccccg cggcgtgcga gtgctccgag gcggcgcgca cggttaagtg cgtgaaccgc 240
aacctgctgg aggtgccggc ggatctaccg ccttacgtgc gcaacctttt ccttaccggc 300
aaccagatga ccgtgctccc cgcgggcgcc ttcgcccgcc agccgccgct cgccgacctg 360
gaggcgctca acctcagcgg caaccacctg aaggaggtgt gtgcaggtgc cttcgagcat 420
ctgccgggtc tgcgccggct tgacctcagc cacaaccctc tcaccaacct cagcgccttc 480
gtctttgcgg gcagcaacgc cagcgtctcg gcccccagcc ccctggagga gctgatcctg 540
aatcacatcg tgccccctga ggatcagagg cagaacggga gcttcgaggg tatggtggcc 600
ttcgaaggca tggtggcagc agctctgcgc tcaggccttg cactccgagg tcttacacgc 660
ctggagctag ccagcaatca ctttcttttc ctgcctcggg acttactagc ccaactgccg 720
agtctcagat acctggacct caggaacaat tccctggtga gcctgaccta cgcatccttc 780
cgcaacctga cacacctcga aagcctccac ttggaggaca atgccctcaa ggtccttcac 840
aactccacct tggctgagtg gcaaggcctg gctcatgtca aggtgttcct ggacaacaat 900
ccctgggttt gcgactgcta catggctgac atggtggctt ggcttaaaga gacagaggtg 960
gtgccagata aagccaggct tacctgcgca ttcccggaga agatgaggaa tcgtggcctc 1020
ttagacctca acagctctga cctggactgt gacgctgtcc ttccccaatc cctgcagact 1080
tcctatgtct tcctaggtat tgttttagct ctgataggcg ctattttcct cctcgttttg 1140
tatttgaacc gtaaaggcat aaaaaagtgg atgcataaca tcagagatgc ctgcagggat 1200
cacatggaag ggtatcatta cagatacgaa atcaatgcgg accccagatt aacaaatctt 1260
agttccaact cggatgtctg a 1281

<210> SEQ ID NO: 3
<211> LENGTH: 901
<212> TYPE: DNA
<213> ORGANISM: Canis sp.
<220> FEATURE:
<221> NAME/KEY: modified_base
<222> LOCATION: (66)
<223> OTHER INFORMATION: a, c, g or t
<221> NAME/KEY: modified_base
<222> LOCATION: (145)
<223> OTHER INFORMATION: a, c, g or t
W--> **89 <221> modified_base**
<222> LOCATION: (277)..(278)
<223> OTHER INFORMATION: a, c, g or t
W--> **92 <221> modified_base**
<222> LOCATION: (287)
<223> OTHER INFORMATION: a, c, g or t
W--> **95 <221> modified_base**

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Input Set : **N:\Crf3\RULE60\10774176.raw**
Output Set: **N:\CRF4\09162004\J774176.raw**

96 <222> LOCATION: (353)
97 <223> OTHER INFORMATION: a, c, g or t
W--> **98 <221> modified_base**
99 <222> LOCATION: (358)
100 <223> OTHER INFORMATION: a, c, g or t
W--> **101 <221> modified_base**
102 <222> LOCATION: (428)..(429)
103 <223> OTHER INFORMATION: a, c, g or t
W--> **104 <221> modified_base**
105 <222> LOCATION: (577)
106 <223> OTHER INFORMATION: a, c, g or t
W--> **107 <221> modified_base**
108 <222> LOCATION: (580)
109 <223> OTHER INFORMATION: a, c, g or t
W--> **110 <221> modified_base**
111 <222> LOCATION: (719)
112 <223> OTHER INFORMATION: a, c, g or t
W--> **113 <221> modified_base**
114 <222> LOCATION: (788)
115 <223> OTHER INFORMATION: a, c, g or t
W--> **116 <221> modified_base**
117 <222> LOCATION: (863)
118 <223> OTHER INFORMATION: a, c, g or t
W--> **119 <221> modified_base**
120 <222> LOCATION: (868)
121 <223> OTHER INFORMATION: a, c, g or t
W--> **122 <221> modified_base**
123 <222> LOCATION: (871)
124 <223> OTHER INFORMATION: a, c, g or t
W--> **125 <400> 3**

126 atcgtgcccc ccgacgaccg gcggcagaac cggagcttcg aggtcatggt ggcggctgcc 60
W--> **127 vddrrnrsvm vaaactccga gcgggccgcg cgcttcgcgg gctgcagtgc ctggagctgg 120**
128 ccggcaaccg cttcragrar gcagnrctct acttgcctcg cgacgtcctg gcccagctac 180
129 ccggcctccg gcacctggac ctgcgcyrdv agrhdraaca attccctggt gagcctcacc 240
130 tacgtgtcct tccgcaacct gacgcacttg gagagcnnsv styvsrnths ctccacctgg 300
131 aggacaacgc cctcaaggtc cttcacaacg ccaccctggc ggagctgcag hdnakvhnat 360
132 aagcctgccc cacgtccggg tcttcctgga caacaacccc tgggtctgcg attgtcacat 420
133 gshvrvdnnw vcdchmgcag acatggtggc ctggctcaag gagacagagg tggtgccggg 480
134 caaagccggg ctcaccadmv awktvvgkag ttgtgcattc ccggagaaaa tgaggaatcg 540
135 ggccctcttg gaactcaaca gctcccacct gcakmrnran sshgactgtg accctatcct 600
136 ccctccatcc ctgcagactt cttatgtctt cctaggtatt gtcdcdstsy vgvttagccc 660
137 tgataggcgc catcttccta ctggttttgt atttgaaccg caaggggata aagagavynr 720
138 kgkaagtgga tgcataacat cagagatgcc tgcagggatc acatggaagg gtatcactac 780
139 agakwmhnrd acrdhmgyhy rtacgaaatc aatgcagacc ccaggttaac aaacctcagt 840
140 tccaattcgg atgtctgaga aynadrtnss nsdvacagtc ggggacagac caaggacaac 900
141 t 901

143 <210> SEQ ID NO: 4
144 <211> LENGTH: 238
145 <212> TYPE: PRT

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Input Set : **N:\Crf3\RULE60\10774176.raw**
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<213> ORGANISM: Canis sp.
<400> SEQUENCE: 4

| | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Ile | Val | Pro | Pro | Asp | Asp | Arg | Arg | Gln | Asn | Arg | Ser | Phe | Glu | Val | Met |
| | 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| | Val | Ala | Ala | Ala | Leu | Arg | Ala | Gly | Arg | Ala | Leu | Arg | Gly | Leu | Gln | Cys |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| | Leu | Glu | Leu | Ala | Gly | Asn | Arg | Phe | Leu | Tyr | Leu | Pro | Arg | Asp | Val | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| | Ala | Gln | Leu | Pro | Gly | Leu | Arg | His | Leu | Asp | Leu | Arg | Asn | Asn | Ser | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| | Val | Ser | Leu | Thr | Tyr | Val | Ser | Phe | Arg | Asn | Leu | Thr | His | Leu | Glu | Ser |
| | 65 | | | | 70 | | | | | 75 | | | | | | 80 |
| | Leu | His | Leu | Glu | Asp | Asn | Ala | Leu | Lys | Val | Leu | His | Asn | Ala | Thr | Leu |
| | | | | 85 | | | | | 90 | | | | | | 95 | |
| | Ala | Glu | Leu | Gln | Ser | Leu | Pro | His | Val | Arg | Val | Phe | Leu | Asp | Asn | Asn |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| | Pro | Trp | Val | Cys | Asp | Cys | His | Met | Ala | Asp | Met | Val | Ala | Trp | Leu | Lys |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| | Glu | Thr | Glu | Val | Val | Pro | Gly | Lys | Ala | Gly | Leu | Thr | Cys | Ala | Phe | Pro |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| | Glu | Lys | Met | Arg | Asn | Arg | Ala | Leu | Leu | Glu | Leu | Asn | Ser | Ser | His | Leu |
| | 145 | | | | 150 | | | | | 155 | | | | | | 160 |
| | Asp | Cys | Asp | Pro | Ile | Leu | Pro | Pro | Ser | Leu | Gln | Thr | Ser | Tyr | Val | Phe |
| | | | | 165 | | | | | 170 | | | | | | 175 | |
| | Leu | Gly | Ile | Val | Leu | Ala | Leu | Ile | Gly | Ala | Ile | Phe | Leu | Leu | Val | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| | Tyr | Leu | Asn | Arg | Lys | Gly | Ile | Lys | Lys | Trp | Met | His | Asn | Ile | Arg | Asp |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| | Ala | Cys | Arg | Asp | His | Met | Glu | Gly | Tyr | His | Tyr | Arg | Tyr | Glu | Ile | Asn |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| | Ala | Asp | Pro | Arg | Leu | Thr | Asn | Leu | Ser | Ser | Asn | Ser | Asp | Val | | |
| | 225 | | | | 230 | | | | | 235 | | | | | | |

<210> SEQ ID NO: 5
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
<400> SEQUENCE: 5

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Phe | Leu | Thr | Gly | Asn | Gln | Leu | Ala | Val |
| | 1 | | | | 5 | | | | |

<210> SEQ ID NO: 6
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
<400> SEQUENCE: 6

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | Ala | Leu | Ile | Gly | Ala | Ile | Phe | Leu | Leu |

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Input Set : **N:\Crf3\RULE60\10774176.raw**
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```
197       1               5
199 <210> SEQ ID NO: 7
200 <211> LENGTH: 9
201 <212> TYPE: PRT
202 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
205 <400> SEQUENCE: 7
206       Ser Leu Gln Thr Ser Tyr Val Phe Leu
207       1               5
209 <210> SEQ ID NO: 8
210 <211> LENGTH: 9
211 <212> TYPE: PRT
212 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
215 <400> SEQUENCE: 8
216       Ala Ile Phe Leu Leu Val Leu Tyr Leu
217       1               5
219 <210> SEQ ID NO: 9
220 <211> LENGTH: 9
221 <212> TYPE: PRT
222 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
225 <400> SEQUENCE: 9
226       Gly Leu Pro His Ile Arg Val Phe Leu
227       1               5
229 <210> SEQ ID NO: 10
230 <211> LENGTH: 9
231 <212> TYPE: PRT
232 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
235 <400> SEQUENCE: 10
236       Phe Leu Gly Ile Val Leu Ala Leu Ile
237       1               5
239 <210> SEQ ID NO: 11
240 <211> LENGTH: 9
241 <212> TYPE: PRT
242 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Description of Artificial Sequence: 5T4 9 Mer
245 <400> SEQUENCE: 11
246       Asn Leu Thr Glu Val Pro Thr Asp Leu
247       1               5
249 <210> SEQ ID NO: 12
250 <211> LENGTH: 9
251 <212> TYPE: PRT
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**RAW SEQUENCE LISTING ERROR SUMMARY** DATE: 09/16/2004
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**Please Note:**
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:3; N Pos. 66,145,277,278,287,353,358,428,429,577,580,719,788,863,868
Seq#:3; N Pos. 871

**VERIFICATION SUMMARY** DATE: 09/16/2004
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Input Set : **N:\Crf3\RULE60\10774176.raw**
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L:89 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:92 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:95 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:98 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:101 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:104 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:107 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:110 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:113 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:116 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:119 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:122 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:125 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:60
M:341 Repeated in SeqNo=3